

A. Delaut

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/147,443D

DATE: 04/17/2001  
TIME: 13:37:07

Input Set : A:\09147443.app  
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3 <110> APPLICANT: Morell, Andreas
4   Imboden, Martin
5   Stadler, Beda
6   Miescher, Sylvia
7   Vogel, Monique
8   Amstutz, Hanspeter
10 <120> TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
11   STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
12   THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
13   PREPARATION AND USE
15 <130> FILE REFERENCE: 6816/P63221US0
17 <140> CURRENT APPLICATION NUMBER: 09/147,443D
18 <141> CURRENT FILING DATE: 1999-01-21
20 <150> PRIOR APPLICATION NUMBER: PCT/EP97/03253
21 <151> PRIOR FILING DATE: 1997-06-20
23 <150> PRIOR APPLICATION NUMBER: EP 96810421.6
24 <151> PRIOR FILING DATE: 1996-06-24
26 <160> NUMBER OF SEQ ID NOS: 79
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 375
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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37 <222> LOCATION: (1)..(375)
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41   Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg
42   1                               5                               10                               15
44   tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat      96
45   Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
46   20                               25                               30
48   gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
49   Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
50   35                               40                               45
52   gca ggt ata tgg ttt gat gga agt aac aaa aac tat gca gac tcc gtg      192
53   Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
54   50                               55                               60
56   aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat      240
57   Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
58   65                               70                               75                               80
60   ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat tgt      288
61   Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
62   85                               90                               95
64   gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac atg      336
65   Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
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66          100          105          110          375
68 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc cca /
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70          115          120          125
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75 <212> TYPE: PRT
76 <213> ORGANISM: Homo sapiens
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82 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
83          20          25          30
85 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
86          35          40          45
88 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
89          50          55          60
91 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
92 65          70          75          80
94 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
95          85          90          95
97 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
98          100          105          110
100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro
101          115          120          125
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106 <211> LENGTH: 318
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens
110 <220> FEATURE:
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112 <222> LOCATION: (1)..(318)
114 <400> SEQUENCE: 3
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117 1          5          10          15
119 gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96
120 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
121          20          25          30
123 tgg tat cag cag aaa cca ggg aaa gcc cct aag ttg ctg atc tat ggt 144
124 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
125          35          40          45
127 gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc 192
128 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
129          50          55          60
131 tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat 240
132 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
133 65          70          75          80
135 ttt gca act tac tac tgt caa gag agt tac agt aat cct cta atc acc 288

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136 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
137                               85                               90                               95
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141                               100                               105
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145 <211> LENGTH: 106
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo sapiens
149 <400> SEQUENCE: 4
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151 1                               5                               10                               15
153 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
154                               20                               25                               30
156 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
157                               35                               40                               45
159 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
160                               50                               55                               60
162 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
163 65                               70                               75                               80
165 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
166                               85                               90                               95
168 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys
169                               100                               105
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174 <211> LENGTH: 375
175 <212> TYPE: DNA
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (1)..(375)
182 <400> SEQUENCE: 5
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184 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
185 1                               5                               10                               15
187 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc gcc ctc aga agt tct 96
188 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
189                               20                               25                               30
191 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
192 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
193                               35                               40                               45
195 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
196 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
197                               50                               55                               60
199 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
201 65                               70                               75                               80
203 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
204 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys

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205          85          90          95
207 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
208 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
209          100          105          110
211 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
212 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
213          115          120          125
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 125
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 6
222 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
223 1 5 10 15
225 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
226 20 25 30
228 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
229 35 40 45
231 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
232 50 55 60
234 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
235 65 70 75 80
237 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
238 85 90 95
240 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
241 100 105 110
243 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
244 115 120 125
248 <210> SEQ ID NO: 7
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251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
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255 <222> LOCATION: (1)..(318)
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260 1 5 10 15
262 gtc acc atc act tgc cgg gca agt cag aac att atc cgc tat tta aat 96
263 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn
264 20 25 30
266 tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt 144
267 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
268 35 40 45
270 gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
271 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
272 50 55 60
274 tct ggg aca gat ttc act ctc acc atc agt agt ctg caa cct gaa gat 240

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275 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
276 65 70 75 80
278 ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act 288
279 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
280 85 90 95
282 ttc ggc cct ggg acc aaa gtg gag atc aaa' 318
283 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
284 100 105
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 106
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
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294 1 5 10 15
296 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn
297 20 25 30
299 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
300 35 40 45
302 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
303 50 55 60
305 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
306 65 70 75 80
308 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
309 85 90 95
311 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
312 100 105
316 <210> SEQ ID NO: 9
317 <211> LENGTH: 375
318 <212> TYPE: DNA
319 <213> ORGANISM: Homo sapiens
321 <220> FEATURE:
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323 <222> LOCATION: (1)..(375)
325 <400> SEQUENCE: 9
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328 1 5 10 15
330 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
331 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
332 20 25 30
334 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
335 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
336 35 40 45
338 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
339 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
340 50 55 60
342 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
343 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

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VERIFICATION SUMMARY

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